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Evaluation of Multi-Environment Forage Yield Trial of Selected Pigeon Pea (*Cajanus cajun*) Genotypes Grown in Western Oromia, Ethiopia Based on GGE Bi-Plot Model

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Abstract: The narrow genetic variability and incidence of new biotic and a biotic stresses have motivated the introduction, evaluation and selection of superior Pigeon pea genotypes for use as forage for livestock in Ethiopia and the western Oromia as well. Identification of high herbage yielding and stable genotype (G) across environment (E) is challenging because of the complete G x E interaction effects. Thus, the current study aimed to analyze forage yielding performance and yield stability of selected Pigeon pea genotypes tested under different environmental conditions of western Oromia, Ethiopia using GGE bi-plot model. The experiment was laid down in randomized complete block design with three replications. Analysis of variance revealed the existence of significant GE interaction for herbage yield trait. The study result indicates that, the magnitude of environment and year main effects and GE interaction for herbage yield of 10 pigeon pea genotypes tested across locations were much lower than genotypic main effects. The GGE bi-plot model also identified promising genotypes based on the mean yield and stability and best environment based on discriminating ability and representativeness. Accordingly, Degagsa and Belabas genotypes were high yielder and showed consistent performance across testing locations and hence recommended for forage production in western Oromia and similar agro-ecologies to the study area. While, Chewaka location provided high information with regard to the genotype difference as compared to the rest locations and thus can be considered as the best sites for growing adapted Pigeon pea genotypes.

Key words: Herbage Yield · Multi-Environment · Representativeness · Stability

INTRODUCTION

In Ethiopia, like other sub Saharan African countries, poor nutrition is a major constraints to livestock production in small holder crop livestock farming, especially during the dry season when available feed quantity and quality extremely poor [1]. Basically this is mainly due to the dependence of livestock on available natural feed resources and little development on forage crops for feeding to animals. According to CSA [2] report, most livestock producers depend largely on natural pasture (54.6%) and crop residue (31.6%) as main sources of feed. Such feed resources are characterized by high fiber, low protein, minerals and vitamins. Such low quality feeds are associated with a low voluntary intake, thus resulting in insufficient nutrient supply, low productivity and even weight loss [3]. This calls for a conscious effort to cultivate improved forages of high quality with high yielding ability, adaptable to biotic and a biotic environmental stress.

To this effect, a range of forage legume species were introduced and evaluated so far under the agro-ecology of Ethiopia and western Oromia as well. Among the improved forage crops introduced, evaluated and promoted in the western part of Oromia, pigeon pea could play an important role in providing a significant amount of biomass yield of 3.36 to 7.22 t/ha with good management practices [4]. The aptness to develop prominent high yielder and stable genotypes over wide environment is an unambiguous motto in pragmatic plant breeding program [5]. In such genotype evaluation trials genotype by environment interaction (GEI) is a common phenomenon [6]. To assess the presence of GEI, however, data from multi-environment trials are necessary for the evaluation

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of yield and genotype adaptability and stability. A genotype or variety is considered to be more adaptive or stable if it has high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environment [7].

Several statistical methodologies for adaptability and stability analyses and to visualize the nature and magnitude of genotype by environment interaction have been described in the literature. Of the methodologies described in varies literatures, genotype and genotype by environment interaction (GGE) bi-plots model was reported as a powerful tool for effective analysis and interpretation of multi-environment data [8]. The GGE bi-plot clearly shows which cultivar won in which environment and thus facilitates mega environment identification. A mega environment is defined as a group of locations that consistently share the same best cultivars [9]. The GGE bi-plot captures both genotype main effects and genotype by environment interaction effects, which are two important sources of variation relevant to genotype evaluation [10].

The herbage yielding potential and other agronomic traits of pigeon pea genotypes tested in the current study were evaluated on a single location, Bako, during the previous preliminary variety trial stage. Genotypes exhibit fluctuating yields when grown in different environment or agro-climatic conditions. Thus, there is a need to undertake further evaluation of these genotypes under varies environmental condition. With this background in mind, the current study was carried to evaluate the herbage yield potential, adaptability and stability of selected pigeon pea genotypes under diverse environmental conditions and finally identifies superior genotype for final verification to be released as a variety

MATERIALS AND METHOD

Description of the Study Locations: The experiment was conducted at three locations (Bako agricultural research center and Gute and Chewaka sub sites) located in western part of Oromia regional state, Ethiopia. The tested locations represents the sub humid mid altitude maize growing area of western Oromia, ranging in altitude from 1259 to 1880 m.a.s.l. Descriptions of all the location are indicated in Table 1.

Table 1: Geographical description of the test locations

	Tested locations		
Parameters	Bako	Chewaka	Gute
Latitude	9°06'N	09° 98285' N	9°01'N
Longitude	37°09'E	036° 11703' E	36°40'E
Altitude (m.a.s.l.)	1650	1259m	1880
Average annual RF (mm)	1431	NI	2067
Average minimum temperature (°C)	11.23	NI	12.2
Average maximum temperature (°C)	31.74	NI	27.9
Soil type	Nitosol	Sandy loam	Clay loam

NI= not identified

Experimental Land Preparation and Planting: Thirty plots, each of which measuring 6 m^2 were established on a single field for uniformity of soil and topography. Experimental sites were properly cleared, ploughed and labeled out for ease of planting. Seeds of pigeon pea genotypes were planted in row at spacing of 1m and 0.5 m between row and plants, respectively. Diammonium phosphate (DAP) fertilizer was applied to all plots during plantation at a rate of 100 kg/ha. Routine experimental management and agronomic practices were carried uniformly at all sites during the course of the study periods.

Experimental Design and Treatments: A two year (2014 and 2015) field study was conducted using 10 accessions of pigeon pea genotypes at three locations (Bako agricultural research center and Billo and Gute sub-sites). The ten genotypes evaluated in the current study were 16274, 16277, 16520, 16524, 16526, 16527, 16528, 16555, 11575 and Tsigab (Standard check). From the genotypes evaluated in the current study; 16527, 11575 and 16555 were selected based on their herbage yielding potential and stability performance and verified against the standard check (Tsigab) in 2016. Then, two of the candidate genotypes (11575 and 16527) were found to be high yielder and stable as compared to the check (Tsigab) and thus released as a variety. The two newly released varieties were named as Degagsa (11575) and Belabas (16527) and hence this naming is used in the entire manuscripts. The experiment was set up using a completely randomized block design with three replications giving a total of 30 observations per sites, respectively.

Sources of Planting Materials: The planting materials used for this study were obtained initially from the so called international livestock center for Africa (ILCA) now the international livestock research institute (ILRI). The pigeon pea genotypes, except the check (Tsigab), evaluated in the presented study were selected from the previous preliminary variety trail carried at Bako based on their herbage yield performance and other agronomic traits.

Data Collection and Measurements: For herbage yield measurement, the middle one rows of each plot were harvested manually with sickle. The fresh weight of the cut biomass was measured just after mowing with suspended field balance and recorded. Then composite sub-samples of 200 g per treatment were taken and oven dried at 65 ºC for 72 h until constant weight attained to determine the herbage dry matter yield in ton per hectare.

Data Analysis: Statistical analysis was done using analysis of variance (ANOVA) following the General Linear Model (GLM) procedure of SAS [11] and significantly different means were separated using least significant difference (LSD) test at 5% level of significance. Genotypes, location, year and their interaction were considered as independent variables in the model for herbage yield measurement. The model used was: $Yijkl= \mu + Gi + Ej + Yk+ (GEY)ijk + Bl(j) + eijkl$, Where; Yijkl = response of measured variables; μ = overall mean; Gi = genotypes effects; Ej = environment effects; (GEY)ijk = interaction effects of genotypes, environment and year; Bl(j)= effects of block l in environment j; eijkl is the random error.

The GGE bi-plot graphic were made by using GENSTAT statistical software package (GenStat, 2012, 15th edition) as described by Yan *et al*. [10] and Yan and kang [6]. The GGE bi-plot graphic analysis was done to generate graphs showing, 1: which won where pattern; 2: ranking of genotypes on the basis of mean yield and stability and 3: an evaluation of the test environment [12].

RESULTS AND DISCUSSION

Output of Combined Analysis of Variance (ANOVA): The result of combined analysis indicates that (Table 2); environments (E), genotypes (G) and years (Y) had highly ($P<0.001$) affected the herbage dry matter yield measurement. With regards to the interaction effects, YGE interaction did not shown significant effects ($P>0.05$) on herbage yield parameters measured. However, interaction of year with genotypes and environment and genotypes with environment had significantly affected the herbage dry matter (DM) yield ($P<0.05$).

The significant GE interaction effects indicated that from statistical point of view, the relative performance of pigeon pea genotypes was not the same across locations, which is not surprising considering the difference in edaphic, climatic and biotic factors among the testing locations. This suggests the need to undertake evaluation of pigeon pea genotypes at multi-locations and years in order to adequately characterize the genotype for difference in forage yield performance.

The partitioning of sum of square revealed that, varietal and environment main effects explained most of the total variation, explaining 75.88 and 12.15% of the total herbage DM yield variation, respectively. The contribution of season/year main effects as well as YG, YE, GE and YGE interaction effects appeared to be negligible for herbage DM yield variation obtained. In disagreement to the current finding where genotypic main effects were more pronounced than either the environment or seasonal main effects as well as interaction attributes, environmental effects was higher than genotype in affecting the DM yield of Napier grass as reported by Gezahegn *et al*. [13]. This variation might be attributed to the genetic variability of the genotype used, agronomic practices applied and climatic condition of test environment.

Herbage Dry Matter (DM) Yield Performance of Pigeon pea across Environments: The mean herbage DM yield of pigeon pea genotypes evaluated at three locations in 2014 and 2015 growing seasons was shown in Table 3. The result revealed that, the herbage DM yield of pigeon

Table 2: Combined analysis of variance for herbage dry matter (DM) yield performance of the ten Pigeon pea genotypes evaluated across locations and years

Sources of variation	Df	SS	MS	Explained SS (%)
Model	61	469.1244322	7.6905645***	-
Year (Y)	1	13.0142222	13.0142222***	2.77
Genotypes (G)	9	355.9799133	39.5533237***	75.88
Environment (E)	2	56.9878878	28.4939439***	12.15
YG	9	5.2932889	0.5881432*	1.13
YE	2	19.2042211	9.6021106***	4.1
GE	18	10.0450567	0.5580587*	2.14
YGE	18	6.9451011	0.3858390^{ns}	1.48
Replication (R)	2	1.6547411	0.8273706^{ns}	0.35
Residual	118	33.6902589	0.2855107	-
Total	179	502.8146911	-	

Table 3: Mean herbage dry matter (DM) (t/ha) yield of selected Pigeon pea genotypes tested across three locations and mean of proportional deviation* of genotype DM yield (%) from corresponding standard check (Tsigab) yield

	2014			2015					
Genotypes	Bk	Chk	Gt	Bk	Chk	Gt	Mean	DM Yield Deviation*	Rank
16274	2.69^{efg}	4.99^{cd}	3.57^{bc}	2.66^{f}	3.37^{c}	2.85^{e}	3.36	-17.44	
16277	2.80^{ef}	4.48^{dc}	4.62^{b}	3.22^{de}	3.58^{c}	2.93^{e}	3.61	-11.47	
16520	2.57^{fg}	5.27^{bc}	3.8^{bc}	2.77^{ef}	3.27^{c}	2.78^{e}	3.41	-16.22	
16524	2.56^{fg}	3.84^{d}	2.91^{c}	3.71^{cd}	3.53^{c}	2.70^{e}	3.21	-21.13	
16526	2.33^{g}	4.53^{cd}	3.53^{bc}	3.60^{cd}	3.31^{c}	2.97^{e}	3.38	-16.95	
16528	3.01^{e}	4.89^{cd}	2.91^{c}	2.57^{f}	2.96^{c}	2.64^{e}	3.16	-22.36	
16555	4.30^{c}	6.47^{b}	5.96^{a}	5.01^{b}	6.21^{b}	4.73^{c}	5.45	33.91	3
Belabas	5.53^{b}	8.16^{a}	6.46^{a}	5.80^{a}	6.95^{ab}	5.51^{b}	6.4	57.25	2
Degagsa	6.39^{a}	9.00^{a}	7.25^{a}	6.27^{a}	7.86^{a}	6.52^{a}	7.22	77.4	1
Tsigab	3.86^{d}	5.42^{bc}	3.71^{bc}	3.91^{c}	3.90^{c}	3.59^{d}	4.07	-	
Mean	3.61	5.71	4.47	3.95	4.49	3.72			
LSD	0.39	1.23	1.29	0.48	1.03	0.44			
CV (%)	6.32	12.6	16.77	7.14	13.32	6.89			

*proportional deviation= (Y-X /X)*100; where Y: accessions mean yield; X: standard check mean yield; BK= bako; Chk= chewaka; Gt= gute; LSD= least significant diference; CV= coefficient of variation; DM= dry matter

pea genotypes had shown significant variation with the testing locations. Despite their difference in magnitude among the locations which in turn depends on the environmental differences, significantly higher herbage DM yield at all testing locations were obtained from genotype named as Degagsa followed by Belabas and 16555. In 2014, the lower herbage DM yield was recorded from 16526 at Bako, 16524 at Chewak and 16528 and 16524 at Gute locations, whereas genotype 16528 was performed lower at all location during the 2015 cropping seasons. The higher herbage DM yield performance of Degagsa, Belabas and 16555 genotypes at all testing locations revealed that, these genotypes are better adapted and performed well as compared to the rest genotypes evaluated. Moreover, this yield difference might be attributed to the genetic variation among the tested genotypes, variability among the testing locations and interaction of genotypes and locations.

Statistically significant variation ($P<0.05$) in herbage DM yield (t/ha) was also observed among the experimental locations, resulting different genotypes to perform differently across the testing locations. Similar finding with the present study result was also reported by Gezahegn *et al.* [13]. Moreover, significantly different yield performance of fourteen grass pea lines across testing locations in Iran were also reported by Ahmadi *et al.* [14]. During both production years, the higher herbage DM yield was obtained from Chewaka location followed by Gute in 2014 and Bako in 2015. The higher herbage DM yield obtained at Chewaka than the other two locations might be resulted due to the uneven distribution of rain fall and soil fertility which is expected to be varied greatly across locations suggesting that Chewaka is better site for growing Pigeon pea for forage purpose as compared to the other study sites. Agro metrological variables [15] such as rainfall, soil and air temperature, wind etc have major impacts on crop growth and development.

In general, with the exception of Degagsa, Belabas and 16555 genotypes which performed higher than standard check (Tsigab), the herbage DM yield performance of the remaining candidate genotypes were lower from that of the check. Accordingly, the mean proportional deviation of accessions` herbage DM yield from the corresponding standard check yield across all testing locations for each genotype (Table 3) revealed that, Degagsa, Belabas and 16555 were emerged as the highest ranked genotypes. These genotypes had yield advantage of 77.4, 57.25 and 33.91% over the standard check (Tsigab) cultivar, respectively and ranked as first, second and third in their herbage yield performance.

GGE Bi-plot Analysis of Herbage Yield Response and Stability of Pigeon pea Genotypes: According to Yan *et al.* [12] report, the GGE refers to the genotype main effect (G) and the genotype by environment interaction effects (GE), which are the two most important sources of variation for cultivar evaluation in multi-environment trials. Thus, for pigeon pea multi-environment forage yield data analysis, the GGE bi-plot is used for which won where pattern; test environment evaluation based on the discriminating ability and representativeness; and genotype evaluation based on the mean performance and stability across mega environment [16].

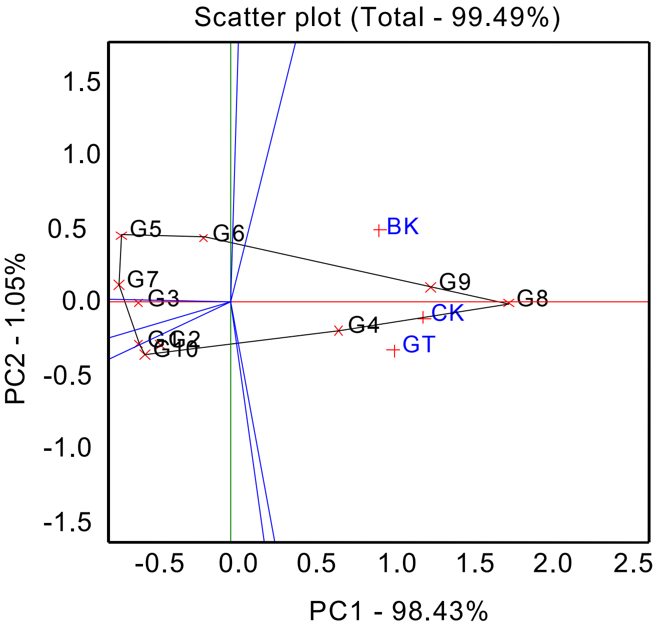

Fig. 1: The " Which won where" pattern view based on genotype by environment interaction herbage yield data of the ten pigeon pea genotypes tested across three locations during 2014 and 2015 cropping seasons. Symbols: **Genotypes**: G1=16274, G2=16277, G3=16526, G4=16555, G5=16524, G6=Tsigab (standard check), G7=16528, G8=Degagsa, G9=Belabas and G10=16520. **Environments**: BK= Bako, GT= Gute and CK= Chewaka

Which Won Where Pattern: The GGE bi-plot graphic analyses of the ten Pigeon pea genotypes tested at three locations are presented in Figure 1. Based on the report of Yan *et al.* [12] the which-won-where pattern of the GGE bi-plot is the most suitable tool for mega environment (Multi environment) data analysis in variety trials. With the present data set, the polygon explained 99.49% of the herbage dry matter yield variation in this study.

The perpendicular lines that make up the polygon by connecting the marker of the pigeon pea genotypes that are furthest away from the bi-plot origin, divide the biplot in to seven sectors. All the environments are found only in one sector implying the target locations had one mega environments, while genotypes are located in five of the sectors. The vertex genotype in each sector represents the highest herbage yielding (Winning) genotype in the location that falls within that particular sector [17]. All the testing locations fell in one sector in which G8 (Degagsa) was the vertex genotype suggesting that this genotype is the best performing one at all testing locations.

The remaining vertex genotypes, G1 (16274), G5 (16524), G6 (Tsigab), G7 (16528) and G10 (16520), without any environment in their sector were not the highest yielding genotypes at any environment rather they were the poorest genotypes of the entire environment. Relative to the vertex genotypes, genotype G2 (16277) and G3 (16526) were located near to the origin of the plot indicating that these genotypes are less responsive than the vertex genotypes [10].

Test Environment Evaluation

Discriminating Ability and Representativeness: In Figure 2, environments are evaluated based on both discriminating ability and representativeness. Multi location trial data can also be used to understand about the test environment besides identifying superior genotypes [12, 18]. Each test environment can be graphically evaluated in a GGE bi-plot for 1) its power to discriminate the genotypes, measured by its length of vectors in the bi-plot and 2) its representativeness of other test environments, measured by its angle with the average environment [19]. Thus, an ideal environment [12] should be both discriminating of the genotypes and representative of the mega environments. Report of Yan *et al.* [12] and Yan [20] indicates that, environment with longer vector is more discriminating of the genotypes than those with the shorter vector length. Based on the fact reported by these authors, the current study result revealed that CK (Chewaka) location provided relatively high information regarding the genotype difference as compared to the remaining locations.

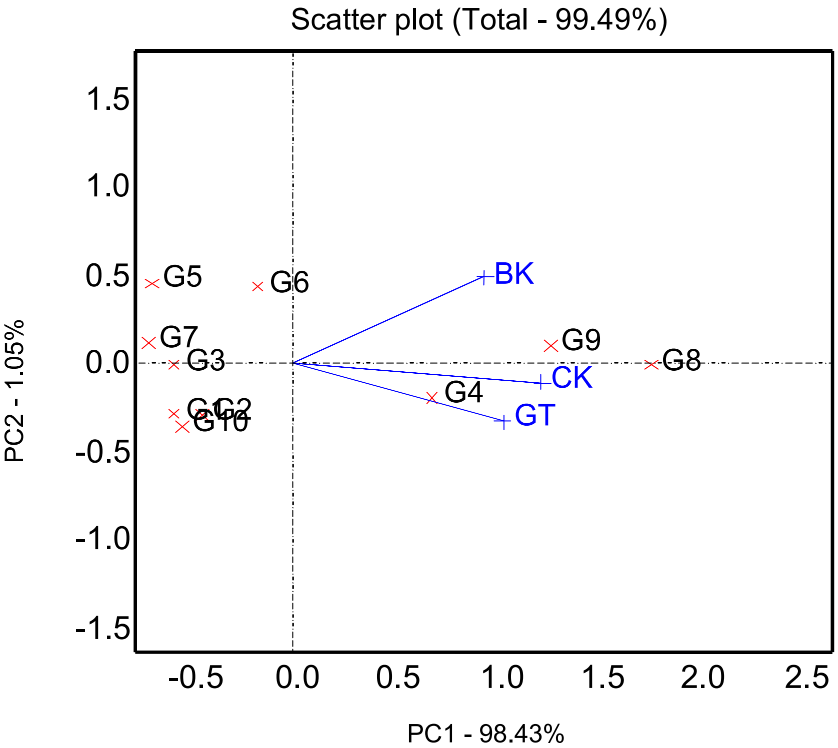

Fig. 2: Discriminating ability and representativeness of the test environments view based on genotypic focused scaling for the mean herbage yield performance and stability of the ten pigeon pea genotypes tested across three locations during 2014 and 2015 cropping seasons. Symbols: **Genotypes**: G1=16274, G2=16277, G3=16526, G4=16555, G5=16524, G6=Tsigab (standard check), G7=16528, G8=Degagsa, G9=Belabas and G10=16520. **Environments**: BK= Bako, GT= Gute and CK= Chewaka

The other most important aspects of test environment evaluation is its representativeness of the mega-environment. Representativeness of the mega environment is visualized by the angle formed between the environment vector and abscissa of average axis. The smaller the angle with the abscissa of average axis, the more representative the environment is Yan and Tinker [21]. Thus, according to the bi-plot display in Figure 2, the most representative environment for pigeon pea genotype cultivation is CK (Chewaka). This suggests that, varieties selected in this location, CK (Chewaka), would have high probability to also perform well in other locations of the same region. In general, based on both discriminating and representativeness characteristics, CK (Chewaka) location was better performed in both aspects and can be considered as good test environment for selecting and growing generally adaptable pigeon pea genotypes.

Genotype Evaluation

Mean Yield Performance and Stability: Visualization of the mean performance and stability of genotypes is always an important issue in cultivar evaluation [6]. These authors further reported that, the average tester coordinate (ATC) is the line that passes through the bi-plot origin and is explained by the average PC1 and PC2 scores of all environments. The result of GGE bi-plot analysis revealed that, the first (PC1) and the second (PC2) principal components explained 98.43 and 1.06% of the total herbage yield variation, respectively making up 98.49 of the total GGE sum of square. In the GGE bi-plot, genotypes with high PC1 (y-axis) scores have high mean yield while those with low PC2 (x-axis) score have stable yield across environments. The average herbage yield of the genotype is approximated by the projection of their marker on the ATC x-axis.

Pigeon pea genotypes with above average mean herbage yield, in the order of G8 (degagsa)>G9 (belabas)>G4 (16555) were selected while other genotypes were discarded. Thus, G8 and G9 were the most stable as well as high yielder genotypes. Even though, G4 was high yielder it was relatively unstable as compared to G8 and G9 genotypes. The superior genotypes or ideal genotype to be released as a variety for effective forage production

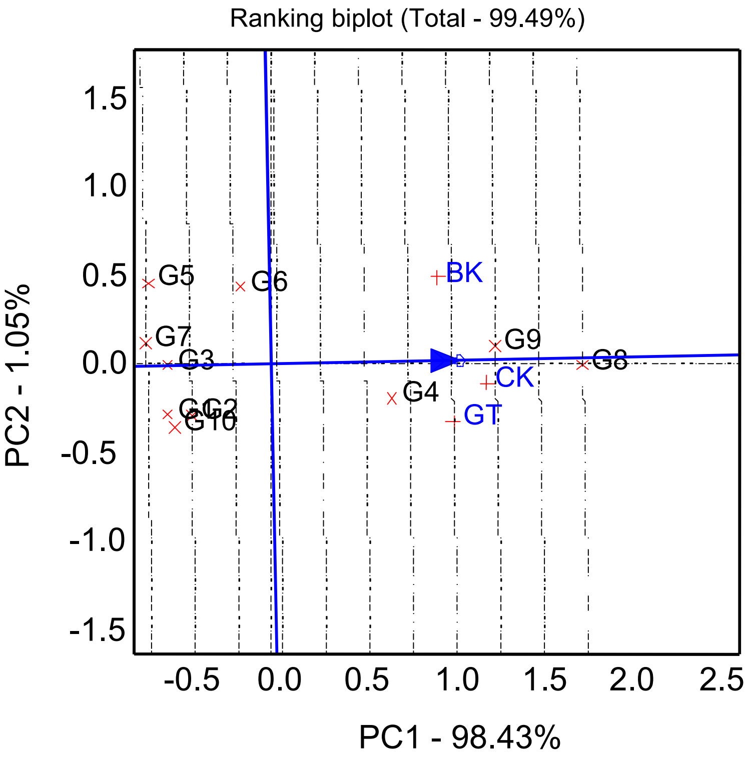

Fig. 3: GGE bi-plot view based on genotypic focused scaling for the mean herbage yield performance and stability of ten pigeon pea genotypes tested across three locations during 2014 and 2015 cropping season. Symbols: **Genotypes**: G1=16274, G2=16277, G3=16526, G4=16555, G5=16524, G6=Tsigab (standard check), G7=16528, G8=Degagsa, G9=Belabas and G10=16520. **Environments**: BK= Bako, GT= Gute and CK= Chewaka

should have both high mean herbage yield and absolutely stable across environments [6]. Hence, G8 and G9 that posses both aspects, a high yield with stable performance across environment, were qualified as the most suitable genotypes among the others, evaluated for herbage production in the western part of Oromia.

CONCLUSION AND RECOMMENDATION

This study made it possible to highlight the herbage yield performance and stability of ten pigeon pea genotypes tested across three locations for two experimental periods. The combined analyses result revealed that, genotype main effect was highly significant explaining 75.88% of the herbage dry matter yield variation than the environment or year main effects as well as interaction effects. Among the tested locations, high herbage dry matter yield was received from Chewaka location in both productions years followed by Gute in 2014 and Bako in 2015. With regard to genotype performance, Degasa, Belabas and 16555 genotypes resulted 77.4, 57.25 and 33.91% herbage yield advantage over the standard check (Tsigab), while the remaining genotypes performed lower than the check. According to the GGE bi-plot models result, G8 (Degagsa) and G9 (Belabas) genotypes were found to be the high herbage dry matter yielder and most stable one across environment than the remaining genotypes evaluated over locations and years and thus can be recommended for cultivation in western Oromia, Ethiopia and similar agro ecologies to the present study area.

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